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Poster *Abstract Submission Form*

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Abstract Text

We have previously established a mechanically coupled, reaction-diffusion model at the tissue scale for predicting breast tumor response to therapy. The 3D model is initialized with patient-specific, quantitative, diffusion-weighted magnetic resonance imaging (DW-MRI) data. Additionally, the model includes a tumor cell reduction term due to chemotherapy drug delivery—estimated using dynamic contrast-enhanced (DCE-) MRI data—following individual patient treatment schedules. One limitation of the current established model is that it does not differentiate between the distinct effects of individual therapies. Therefore, to extend this model to explicitly include the effects of specific systemic therapies, we turn to *in vitro* data collected for breast cancer response at the cellular scale (measured by time-resolved microscopy) to initialize and constrain a multi-scale model of treatment response. This requires interlacing experimental data and additional expressions into the tissue scale model to represent drug dynamics at the cellular scale to simulate overall tumor response. Our aim is to leverage tumor cell response data to individual drugs to not only improve the overall predictive ability of the clinical model but also to explore alternative therapeutic strategies. We propose that an integrated multi-scale mathematical-experimental approach bridging tissue and cellular scale data can elucidate the optimal strategies for combination therapy for breast cancer.